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# PUG SOAP Web Service Reference

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## Table of Contents

<b>PUG SOAP Web Service Reference.....</b>	<b>1</b>
PUG SOAP Web Service.....	2
Methods.....	3
Complex Types.....	36
Simple Types.....	52

# Overview

## Description

This document contains Web Service descriptions for the following services.

## Web Services

Name	Description
PUG SOAP	

## PUG SOAP Web Service

### See Also

[Methods](#) | [Complex Types](#) | [Simple Types](#)

## Methods: PUG SOAP

### Methods

Name	Description
AssayDownload	Given an assay key, prepare for download a file containing an assay data table in the selected format. See the assay query section of the PUG service documentation ( <a href="http://pubchem.ncbi.nlm.nih.gov/pug/pughelp.html">http://pubchem.ncbi.nlm.nih.gov/pug/pughelp.html</a> ) for more detail on the supported formats. Compression is optional and defaults to gzip (.gz). Returns a download key. Asynchronous.
Download	Given a list key, prepare for download a file containing those records in the selected format. See the web download service documentation ( <a href="http://pubchem.ncbi.nlm.nih.gov/pc_fetch/pc_fetch-help.html">http://pubchem.ncbi.nlm.nih.gov/pc_fetch/pc_fetch-help.html</a> ) for more detail on the supported formats and file types. Returns a download key. Asynchronous. Note that if SynchronousSingleRecord is set to true, and the ListKey contains only a single ID, then a Base64 string of data is returned synchronously in the response, instead of going through the download file.
GetAssayColumnDescription	Get the description of column (readout) in a BioAssay, which may be the outcome, score, or a TID from the given AID. Synchronous.
GetAssayColumnDescriptions	Get the description of all columns (readouts) in a BioAssay. Synchronous.
GetAssayDescription	Get the descriptive information for a BioAssay, including the number of user-specified readouts (TIDs) and whether a score readout is present. Optionally get version and SID/CID count information. If GetFullDataBlob is set to true, then a Base64 string of data is returned in the response instead, containing the full PubChem Assay description in the requested format (ASN or XML only). Synchronous.
GetDownloadUrl	Given a download key, return an FTP URL that may be used to download the requested file. Synchronous.
GetEntrezKey	Given a list key, return an Entrez history key (db, query key, and WebEnv) corresponding to that list. Synchronous.
GetEntrezUrl	Given an Entrez history key (db, query key, and WebEnv), return an HTTP URL that may be used to view the list in Entrez. Synchronous.
GetIDList	Given a list key, return the identifiers as an array of integers. Synchronous.
GetListItemsCount	Return the number of IDs in the set represented by the given list key. Synchronous.
GetOperationStatus	Given a key for any asynchronous operation, return the status of that operation. Possible return values are: Success, the operation completed normally; HitLimit, TimeLimit: the operation finished normally, but one of the limits was reached (e.g. before the entire database was searched); ServerError, InputError, DataError, Stopped: there was a problem with the input or on the server, and the job has died; Queued: the operation is waiting its turn in the public queue; Running: the operation is in progress. Synchronous.
GetStandardizedCID	Given a structure key that has been processed by Standardize, return the corresponding PubChem Compound database CID, or an empty value if the structure is not present in PubChem. Synchronous.

Name	Description
GetStandardizedStructure	Given a structure key that has been processed by Standardize, return the chemical structure in as SMILES or InChI strings. Synchronous.
GetStandardizedStructureBase64	Given a structure key that has been processed by Standardize, return the chemical structure as ASN, XML, or SDF, returned as a Base64-encoded string. Synchronous.
GetStatusMessage	Given a key for any asynchronous operation, return any system messages (error messages, job info, etc.) associated with the operation, if any. Synchronous.
IdentitySearch	Search PubChem Compound for structures identical to the one given by the structure key input, based on a user-selected level of chemical identity: connectivity only, match isotopes and/or stereo, etc. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.
IDExchange	Convert IDs from one type to another, using any one of a variety of CID matching algorithms. Output can be a list or a downloaded file; download file compression is optional and defaults to gzip (.gz). Returns a list or download key. Asynchronous.
InputAssay	Specify an assay table from a BioAssay AID. The table may be complete, concise, or include a ListKey-specified set of readouts (TIDs). By default, all tested substances are included, but can be restricted to a ListKey-specified set of SIDs or CIDs. Returns an assay key. Synchronous.
InputEntrez	Input an Entrez history key (db, query key, and WebEnv). Returns a list key. Synchronous.
InputList	Input a set of identifiers for a PubChem database, as an array of integers. Returns a list key. Synchronous.
InputListString	Input a set of identifiers for a PubChem database, as an array of strings. Returns a list key. Synchronous.
InputListItemText	Input a set of identifiers for a PubChem database, as a simple string of integer values separated by commas and/or whitespace. Returns a list key. Synchronous.
InputStructure	Input a chemical structure as a simple (one-line) string, either SMILES or InChI. Returns a structure key. Synchronous.
InputStructureBase64	Input a chemical structure in ASN.1 (text or binary), XML, or SDF format. The structure must be encoded as a Base64 string. Currently only single structures are supported. Returns a structure key. Synchronous.
MFSearch	Search PubChem Compound for structures of a given molecular formula, optionally allowing elements not specified to be present. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.
ScoreMatrix	Compute a matrix of scores from one or two lists of IDs (if one, the IDs will be self-scored), of the selected type and in the selected format. Compression is optional and defaults to gzip (.gz). Returns a download key. Asynchronous.

## Methods

Name	Description
SimilaritySearch2D	Search PubChem Compound for structures similar to the one given by the structure key input, based on the given Tanimoto-based similarity score. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.
Standardize	Standardize the structure given by the structure key input, using the same algorithm PubChem uses to construct the Compound database. Returns a structure key. Asynchronous.
SubstructureSearch	Search PubChem Compound for structures containing the one given by the structure key input, based on a user-selected level of chemical identity: connectivity only, match isotopes and/or stereo, etc. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.
SuperstructureSearch	Search PubChem Compound for structures contained within the one given by the structure key input, based on a user-selected level of chemical identity: connectivity only, match isotopes and/or stereo, etc. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.

## Method: AssayDownload

### Description

Given an assay key, prepare for download a file containing an assay data table in the selected format. See the assay query section of the PUG service documentation (<http://pubchem.ncbi.nlm.nih.gov/pug/pughelp.html>) for more detail on the supported formats. Compression is optional and defaults to gzip (.gz). Returns a download key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/AssayDownload>

### Input

The input of this method is the argument AssayDownload having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AssayKey	s:string	1..1
tns:AssayFormat	tns:AssayFormatType	1..1
tns:eCompress	tns:CompressType	0..1

### Output

The output of this method is the argument AssayDownloadResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:DownloadKey	s:string	1..1

## Method: Download

### Description

Given a list key, prepare for download a file containing those records in the selected format. See the web download service documentation ([http://pubchem.ncbi.nlm.nih.gov/pc\\_fetch/pc\\_fetch-help.html](http://pubchem.ncbi.nlm.nih.gov/pc_fetch/pc_fetch-help.html)) for more detail on the supported formats and file types. Returns a download key. Asynchronous. Note that if SynchronousSingleRecord is set to true, and the ListKey contains only a single ID, then a Base64 string of data is returned synchronously in the response, instead of going through the download file.

### Action

<http://pubchem.ncbi.nlm.nih.gov/Download>

### Input

The input of this method is the argument Download having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1
tns>eFormat	tns:FormatType	1..1
tns>eCompress	tns:CompressType	0..1
tns>Use3D	s:boolean	0..1
tns>N3DConformers	s:int	0..1
tns>SynchronousSingleRecord	s:boolean	0..1

### Output

The output of this method is the argument DownloadResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>DownloadKey	s:string	0..1
tns>DataBlob	tns>DataBlobType	0..1

## Method: GetAssayColumnDescription

### Description

Get the description of column (readout) in a BioAssay, which may be the outcome, score, or a TID from the given AID. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetAssayColumnDescription>

### Input

The input of this method is the argument GetAssayColumnDescription having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AID	s:int	1..1
tns:Heading	tns:HeadingType	1..1
tns:TID	s:int	0..1

### Output

The output of this method is the argument GetAssayColumnDescriptionResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:ColumnDescription	tns:ColumnDescriptionType	1..1

## Method: GetAssayColumnDescriptions

### Description

Get the description of all columns (readouts) in a BioAssay. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetAssayColumnDescriptions>

### Input

The input of this method is the argument GetAssayColumnDescriptions having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AID	s:int	1..1

### Output

The output of this method is the argument GetAssayColumnDescriptionsResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:ColumnDescription	tns:ColumnDescriptionType	1..*

## Method: GetAssayDescription

### Description

Get the descriptive information for a BioAssay, including the number of user-specified readouts (TIDs) and whether a score readout is present. Optionally get version and SID/CID count information. If GetFullDataBlob is set to true, then a Base64 string of data is returned in the response instead, containing the full PubChem Assay description in the requested format (ASN or XML only). Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetAssayDescription>

### Input

The input of this method is the argument GetAssayDescription having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AID	s:int	1..1
tns:GetVersion	s:boolean	0..1
tns:GetCounts	s:boolean	0..1
tns:GetFullDataBlob	s:boolean	0..1
tns:eFormat	tns:FormatType	0..1

### Output

The output of this method is the argument GetAssayDescriptionResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AssayDescription	tns:AssayDescriptionType	0..1
tns:DataBlob	tns:DataBlobType	0..1

## Method: GetDownloadUrl

### Description

Given a download key, return an FTP URL that may be used to download the requested file. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetDownloadUrl>

### Input

The input of this method is the argument GetDownloadUrl having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:DownloadKey	s:string	1..1

### Output

The output of this method is the argument GetDownloadUrlResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:url	s:string	1..1

## Method: GetEntrezKey

### Description

Given a list key, return an Entrez history key (db, query key, and WebEnv) corresponding to that list.  
Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetEntrezKey>

### Input

The input of this method is the argument GetEntrezKey having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

### Output

The output of this method is the argument GetEntrezKeyResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:EntrezKey	tns:EntrezKey	1..1

## Method: GetEntrezUrl

### Description

Given an Entrez history key (db, query key, and WebEnv), return an HTTP URL that may be used to view the list in Entrez. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetEntrezUrl>

### Input

The input of this method is the argument GetEntrezUrl having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:EntrezKey	tns:EntrezKey	1..1

### Output

The output of this method is the argument GetEntrezUrlResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:url	s:string	1..1

## Method: GetIDList

### Description

Given a list key, return the identifiers as an array of integers. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetIDList>

### Input

The input of this method is the argument GetIDList having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1
tns Start	s:int	0..1
tns>Count	s:int	0..1

### Output

The output of this method is the argument GetIDListResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>IDList	tns:ArrayOfInt	1..1

## Method: GetListItemsCount

### Description

Return the number of IDs in the set represented by the given list key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetListItemsCount>

### Input

The input of this method is the argument GetListItemsCount having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

### Output

The output of this method is the argument GetListItemsCountResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>count	s:int	1..1

## Method: GetOperationStatus

### Description

Given a key for any asynchronous operation, return the status of that operation. Possible return values are: Success, the operation completed normally; HitLimit, TimeLimit: the operation finished normally, but one of the limits was reached (e.g. before the entire database was searched); ServerError, InputError, DataError, Stopped: there was a problem with the input or on the server, and the job has died; Queued: the operation is waiting its turn in the public queue; Running: the operation is in progress. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetOperationStatus>

### Input

The input of this method is the argument GetOperationStatus of type tns:AnyKeyType having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AnyKey	s:string	1..1

### Output

The output of this method is the argument GetOperationStatusResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:status	tns>StatusType	1..1

## Method: GetStandardizedCID

### Description

Given a structure key that has been processed by Standardize, return the corresponding PubChem Compound database CID, or an empty value if the structure is not present in PubChem. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetStandardizedCID>

### Input

The input of this method is the argument GetStandardizedCID having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1

### Output

The output of this method is the argument GetStandardizedCIDResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:CID	s:int	1..1

## Method: GetStandardizedStructure

### Description

Given a structure key that has been processed by Standardize, return the chemical structure in as SMILES or InChI strings. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetStandardizedStructure>

### Input

The input of this method is the argument GetStandardizedStructure having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1
tns:format	tns:FormatType	1..1

### Output

The output of this method is the argument GetStandardizedStructureResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:structure	s:string	1..1

## Method: GetStandardizedStructureBase64

### Description

Given a structure key that has been processed by Standardize, return the chemical structure as ASN, XML, or SDF, returned as a Base64-encoded string. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetStandardizedStructureBase64>

### Input

The input of this method is the argument GetStandardizedStructureBase64 having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1
tns:format	tns:FormatType	1..1

### Output

The output of this method is the argument GetStandardizedStructureBase64Response having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:structure	s:base64Binary	1..1

## Method: GetStatusMessage

### Description

Given a key for any asynchronous operation, return any system messages (error messages, job info, etc.) associated with the operation, if any. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/GetStatusMessage>

### Input

The input of this method is the argument GetStatusMessage of type tns:AnyKeyType having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AnyKey	s:string	1..1

### Output

The output of this method is the argument GetStatusMessageResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:message	s:string	1..1

## Method: IdentitySearch

### Description

Search PubChem Compound for structures identical to the one given by the structure key input, based on a user-selected level of chemical identity: connectivity only, match isotopes and/or stereo, etc. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/IdentitySearch>

### Input

The input of this method is the argument IdentitySearch having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1
tns:idOptions	tns:IdentitySearchOptions	1..1
tns:limits	tns:LimitsType	0..1

### Output

The output of this method is the argument IdentitySearchResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: IDExchange

### Description

Convert IDs from one type to another, using any one of a variety of CID matching algorithms. Output can be a list or a downloaded file; download file compression is optional and defaults to gzip (.gz). Returns a list or download key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/IDExchange>

### Input

The input of this method is the argument IDExchange having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:InputListKey	s:string	1..1
tns:Operation	tns:IDOperationType	1..1
tns:OutputType	tns:PCIDType	1..1
tns:OutputSourceName	s:string	0..1
tns:OutputFormat	tns:IDOutputFormatType	1..1
tns:ToWebEnv	s:string	0..1
tns:eCompress	tns:CompressType	0..1

### Output

The output of this method is the argument IDExchangeResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	0..1
tns:DownloadKey	s:string	0..1

## Method: InputAssay

### Description

Specify an assay table from a BioAssay AID. The table may be complete, concise, or include a ListKey-specified set of readouts (TIDs). By default, all tested substances are included, but can be restricted to a ListKey-specified set of SIDs or CIDs. Returns an assay key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputAssay>

### Input

The input of this method is the argument InputAssay having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AID	s:int	1..1
tns:Columns	tns:AssayColumnsType	1..1
tns>ListKeyTIDs	s:string	0..1
tns>ListKeySCIDs	s:string	0..1
tns:OutcomeFilter	tns:AssayOutcomeFilterType	0..1

### Output

The output of this method is the argument InputAssayResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:AssayKey	s:string	1..1

## Method: InputEntrez

### Description

Input an Entrez history key (db, query key, and WebEnv). Returns a list key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputEntrez>

### Input

The input of this method is the argument InputEntrez having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:EntrezKey	tns:EntrezKey	1..1

### Output

The output of this method is the argument InputEntrezResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: InputList

### Description

Input a set of identifiers for a PubChem database, as an array of integers. Returns a list key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputList>

### Input

The input of this method is the argument InputList having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:ids	tns:ArrayOfInt	1..1
tns:idType	tns:PCIDType	1..1

### Output

The output of this method is the argument InputListResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: InputListString

### Description

Input a set of identifiers for a PubChem database, as an array of strings. Returns a list key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputListString>

### Input

The input of this method is the argument InputListString having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:strids	tns:ArrayOfString	1..1
tns:idType	tns:PCIDType	1..1
tns:SourceName	s:string	0..1

### Output

The output of this method is the argument InputListStringResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: InputListText

### Description

Input a set of identifiers for a PubChem database, as a simple string of integer values separated by commas and/or whitespace. Returns a list key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputListText>

### Input

The input of this method is the argument InputListText having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:ids	s:string	1..1
tns:idType	tns:PCIDType	1..1

### Output

The output of this method is the argument InputListTextResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: InputStructure

### Description

Input a chemical structure as a simple (one-line) string, either SMILES or InChI. Returns a structure key.  
Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputStructure>

### Input

The input of this method is the argument InputStructure having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:structure	s:string	1..1
tns:format	tns:FormatType	1..1

### Output

The output of this method is the argument InputStructureResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1

## Method: InputStructureBase64

### Description

Input a chemical structure in ASN.1 (text or binary), XML, or SDF format. The structure must be encoded as a Base64 string. Currently only single structures are supported. Returns a structure key. Synchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/InputStructureBase64>

### Input

The input of this method is the argument InputStructureBase64 having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:structure	s:base64Binary	1..1
tns:format	tns:FormatType	1..1

### Output

The output of this method is the argument InputStructureBase64Response having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1

## Method: MFSearch

### Description

Search PubChem Compound for structures of a given molecular formula, optionally allowing elements not specified to be present. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/MFSearch>

### Input

The input of this method is the argument MFSearch having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:MF	s:string	1..1
tns:mfOptions	tns:MFSearchOptions	0..1
tns:limits	tns:LimitsType	0..1

### Output

The output of this method is the argument MFSearchResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: ScoreMatrix

### Description

Compute a matrix of scores from one or two lists of IDs (if one, the IDs will be self-scored), of the selected type and in the selected format. Compression is optional and defaults to gzip (.gz). Returns a download key.  
Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/ScoreMatrix>

### Input

The input of this method is the argument ScoreMatrix having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1
tnsSecondaryListKey	s:string	0..1
tnsScoreType	tnsScoreTypeType	1..1
tnsMatrixFormat	tnsMatrixFormatType	1..1
tnsECompress	tnsCompressType	0..1
tnsN3DConformers	s:int	0..1
tnsNo3DParent	s:boolean	0..1

### Output

The output of this method is the argument ScoreMatrixResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tnsDownloadKey	s:string	1..1

## Method: SimilaritySearch2D

### Description

Search PubChem Compound for structures similar to the one given by the structure key input, based on the given Tanimoto-based similarity score. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/SimilaritySearch2D>

### Input

The input of this method is the argument SimilaritySearch2D having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1
tns:simOptions	tns:SimilaritySearchOptions	1..1
tns:limits	tns:LimitsType	0..1

### Output

The output of this method is the argument SimilaritySearch2DResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: Standardize

### Description

Standardize the structure given by the structure key input, using the same algorithm PubChem uses to construct the Compound database. Returns a structure key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/Standardize>

### Input

The input of this method is the argument Standardize having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1

### Output

The output of this method is the argument StandardizeResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1

## Method: SubstructureSearch

### Description

Search PubChem Compound for structures containing the one given by the structure key input, based on a user-selected level of chemical identity: connectivity only, match isotopes and/or stereo, etc. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/SubstructureSearch>

### Input

The input of this method is the argument SubstructureSearch having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1
tns:ssOptions	tns:StructureSearchOptions	0..1
tns:limits	tns:LimitsType	0..1

### Output

The output of this method is the argument SubstructureSearchResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Method: SuperstructureSearch

### Description

Search PubChem Compound for structures contained within the one given by the structure key input, based on a user-selected level of chemical identity: connectivity only, match isotopes and/or stereo, etc. The search may be limited by elapsed time or number of records found, or restricted to search only within a previous result set (given by a list key). Returns a list key. Asynchronous.

### Action

<http://pubchem.ncbi.nlm.nih.gov/SuperstructureSearch>

### Input

The input of this method is the argument SuperstructureSearch having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns:StrKey	s:string	1..1
tns:ssOptions	tns:StructureSearchOptions	0..1
tns:limits	tns:LimitsType	0..1

### Output

The output of this method is the argument SuperstructureSearchResponse having the structure defined by the following table.

Element	Type	Occurs
SEQUENCE		1..1
tns>ListKey	s:string	1..1

## Complex Types: PUG SOAP

### Complex Types

Name
tns:AnyKeyType
tns:ArrayOfInt
tns:ArrayOfString
tns:ArrayOfTargets
tns:AssayDescriptionType
tns:AssayTargetType
tns:ColumnDescriptionType
tns:DataBlobType
tns:EntrezKey
tns:IdentitySearchOptions
tns:LimitsType
tns:MFSearcOptions
tns:SimilaritySearchOptions
tns:StructureSearchOptions
tns:TestedConcentrationType

## Complex Type: tns:AnyKeyType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:AnyKey	s:string	1..1

## Complex Type: tns:ArrayOfInt

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:int	s:int	1..*

## Complex Type: tns:ArrayOfString

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:string	s:string	1..*

## Complex Type: tns:ArrayOfTargets

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:Target	tns:AssayTargetType	1..*

## Complex Type: tns:AssayDescriptionType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:Name	s:string	0..1
tns:Description	tns:ArrayOfString	0..1
tns:Protocol	tns:ArrayOfString	0..1
tns:Comment	tns:ArrayOfString	0..1
tns:NumberOfTIDs	s:int	1..1
tns:HasScore	s:boolean	1..1
tns:Method	s:string	0..1
tns:Targets	tns:ArrayOfTargets	0..1
tns:Version	s:int	0..1
tns:Revision	s:int	0..1
tns:LastDataChange	s:int	0..1
tns:SIDCountAll	s:int	0..1
tns:SIDCountActive	s:int	0..1
tns:SIDCountInactive	s:int	0..1
tns:SIDCountInconclusive	s:int	0..1
tns:SIDCountUnspecified	s:int	0..1
tns:SIDCountProbe	s:int	0..1
tns:CIDCountAll	s:int	0..1
tns:CIDCountActive	s:int	0..1
tns:CIDCountInactive	s:int	0..1
tns:CIDCountInconclusive	s:int	0..1
tns:CIDCountUnspecified	s:int	0..1
tns:CIDCountProbe	s:int	0..1

## Complex Type: tns:AssayTargetType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:gi	s:int	1..1
tns:Name	s:string	0..1

## Complex Type: tns:ColumnDescriptionType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:Heading	tns:HeadingType	1..1
tns:TID	s:int	0..1
tns:Name	s:string	1..1
tns:Description	tns:ArrayOfString	0..1
tns:Type	s:string	1..1
tns:Unit	s:string	0..1
tns:TestedConcentration	tns:TestedConcentrationType	0..1
tns:ActiveConcentration	s:boolean	0..1

## Complex Type: tns:DataBlobType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:Data	s:base64Binary	1..1
tns:BlobFormat	tns:BlobFormatType	0..1
tns:eCompress	tns:CompressType	0..1

## Complex Type: tns:EntrezKey

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:db	s:string	1..1
tns:key	s:string	1..1
tns:webenv	s:string	1..1

## Complex Type: tns:IdentitySearchOptions

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:elidentity	tns:IdentityType	1..1
tns:ToWebEnv	s:string	0..1

## Complex Type: tns:LimitsType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:seconds	s:int	0..1
tns:maxRecords	s:int	0..1
tns>ListKey	s:string	0..1

## Complex Type: tns:MFSearchOptions

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:AllowOtherElements	s:boolean	1..1
tns:ToWebEnv	s:string	0..1

## Complex Type: tns:SimilaritySearchOptions

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:threshold	s:int	1..1
tns:ToWebEnv	s:string	0..1

## Complex Type: tns:StructureSearchOptions

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:MatchIsotopes	s:boolean	0..1
tns:MatchCharges	s:boolean	0..1
tns:MatchTautomers	s:boolean	0..1
tns:RingsNotEmbedded	s:boolean	0..1
tns:SingeDoubleBondsMatch	s:boolean	0..1
tns:ChainsMatchRings	s:boolean	0..1
tns:StripHydrogen	s:boolean	0..1
tns:eStereo	tns:STEREOTYPE	0..1
tns:ToWebEnv	s:string	0..1

## Complex Type: tns:TestedConcentrationType

### Derived By

Restricting s:anyType

### Content Model

Contains elements as defined in the following table.

Component	Type	Occurs
SEQUENCE		1..1
tns:Concentration	s:double	1..1
tns:Unit	s:string	1..1

## Simple Types: PUG SOAP

### Simple Types

Name
tns:AssayColumnsType
tns:AssayFormatType
tns:AssayOutcomeFilterType
tns:BlobFormatType
tns:CompressType
tns:FormatType
tns:HeadingType
tns:IdentityType
tns:IDOperationType
tns:IDOutputFormatType
tns:MatrixFormatType
tns:PCIDType
tns:ScoreTypeType
tns:StatusType
tns:StereoType

## Simple Type: tns:AssayColumnsType

### Derived By

Restricting s:string

### Enumeration

Value
eAssayColumns_Complete
eAssayColumns_Concise
eAssayColumns_TIDs

## Simple Type: tns:AssayFormatType

### Derived By

Restricting s:string

### Enumeration

Value
eAssayFormat_XML
eAssayFormat ASN Text
eAssayFormat ASN Binary
eAssayFormat CSV

## Simple Type: tns:AssayOutcomeFilterType

### Derived By

Restricting s:string

### Enumeration

Value
eAssayOutcome_All
eAssayOutcome_Inactive
eAssayOutcome_Active
eAssayOutcome_Inconclusive
eAssayOutcome_Unspecified

## Simple Type: tns:BlobFormatType

### Derived By

Restricting s:string

### Enumeration

Value
eBlobFormat_Unspecified
eBlobFormat_ASNB
eBlobFormat_ASNT
eBlobFormat_XML
eBlobFormat_SDF
eBlobFormat_CSV
eBlobFormat_Text
eBlobFormat_HTML
eBlobFormat_PNG
eBlobFormat_Other

## Simple Type: tns:CompressType

### Derived By

Restricting s:string

### Enumeration

Value
eCompress_None
eCompress_GZip
eCompress_BZip2

## Simple Type: tns:FormatType

### Derived By

Restricting s:string

### Enumeration

Value
eFormat_ASNB
eFormat_ASNT
eFormat_XML
eFormat_SDF
eFormat_SMILES
eFormat_InChI
eFormat_Image
eFormat_Thumbnail

## Simple Type: tns:HeadingType

### Derived By

Restricting s:string

### Enumeration

Value
TID
outcome
score

## Simple Type: tns:IdentityType

### Derived By

Restricting s:string

### Enumeration

Value
elidentity_SameConnectivity
elidentity_AnyTautomer
elidentity_SameStereo
elidentity_SameIsotope
elidentity_SameStereoIsotope
elidentity_SameNonconflictStereo
elidentity_SameIsotopeNonconflictStereo

## Simple Type: tns:IDOperationType

### Derived By

Restricting s:string

### Enumeration

Value
eIDOperation_Same
eIDOperation_SameStereo
eIDOperation_SameIsotope
eIDOperation_SameConnectivity
eIDOperation_SameParent
eIDOperation_SameParentStereo
eIDOperation_SameParentIsotope
eIDOperation_SameParentConnectivity
eIDOperation_Similar2D
eIDOperation_Similar3D

## Simple Type: tns:IDOutputFormatType

### Derived By

Restricting s:string

### Enumeration

Value
eIDOutputFormat_Entrez
eIDOutputFormat_FileList
eIDOutputFormat_FilePair

## Simple Type: tns:MatrixFormatType

### Derived By

Restricting s:string

### Enumeration

Value
eMatrixFormat_CSV
eMatrixFormat_IdIdScore

## Simple Type: tns:PCIDType

### Derived By

Restricting s:string

### Enumeration

Value
eID_CID
eID_SID
eID_AID
eID_TID
eID_ConformerID
eID_SourceID
eID_InChI
eID_InChIKey

## Simple Type: tns:ScoreTypeType

### Derived By

Restricting s:string

### Enumeration

Value
eScoreType_Sim2DSubs
eScoreType_ShapeOpt3D
eScoreType_FeatureOpt3D

## Simple Type: tns:StatusType

### Derived By

Restricting s:string

### Enumeration

Value
eStatus_Unknown
eStatus_Success
eStatus_ServerError
eStatus_HitLimit
eStatus_TimeLimit
eStatus_InputError
eStatus_DataError
eStatus_Stopped
eStatus_Running
eStatus_Queued

## Simple Type: tns: StereoType

### Derived By

Restricting s:string

### Enumeration

Value
eStereo_Ignore
eStereo_Exact
eStereo_Relative
eStereo_NonConflicting

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# Index

**A**

AnyKeyType	37	GetAssayColumnDescriptions	9
ArrayOfInt	38	GetAssayDescription	10
ArrayOfString	39	GetDownloadUrl	11
ArrayOfTargets	40	GetEntrezKey	12
AssayColumnsType	53	GetEntrezUrl	13
AssayDescriptionType	41	GetIDList	14
AssayDownload	6	GetListItemsCount	15
AssayFormatType	54	GetOperationStatus	16
AssayOutcomeFilterType	55	GetStandardizedCID	17
AssayTargetType	42	GetStandardizedStructure	18
		GetStandardizedStructureBase64	19
		4	
		GetStatusMessage	20

**B**

BlobFormatType	56
----------------	----

**C**

ColumnDescriptionType	43
Complex Types	36
CompressType	57

**D**

DataBlobType	44
Download	7

**E**

EntrezKey	45
-----------	----

**F**

FormatType	58
------------	----

**G**

GetAssayColumnDescription	8
---------------------------	---

**H**

HeadingType	59
-------------	----

**I**

IdentitySearch	21
IdentitySearchOptions	46
IdentityType	60
IDExchange	22
IDOperationType	61
IDOutputFormatType	62
InputAssay	23
InputEntrez	24
InputList	25
InputListString	26
InputListItemText	27
InputStructure	28
InputStructureBase64	29

**L**

LimitsType	47	ScoreTypeType	65
		SimilaritySearch2D	32
<b>M</b>		SimilaritySearchOptions	49
MatrixFormatType	63	Simple Types	52
Methods	3	Standardize	33
MFSearch	30	StatusType	66
MFSearchOptions	48	StereoType	67
		StructureSearchOptions	50
<b>P</b>		SubstructureSearch	34
PCIDType	64	SuperstructureSearch	35
PUG SOAP Web Service	2		
<b>S</b>		TestedConcentrationType	51
ScoreMatrix	31		

**T**